

GenCore version 5.1.3
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OM nucleic - nucleic search, using sw model

Run on: January 14, 2003, 11:42:22, Search time 4172.38 seconds

(without alignment)
11136.303 Million cell updates/sec

Title: US-09-910-428-3

Perfect score: 2869

Sequence: 1 ctcgagatccctctgctgctg aataagaagattatagctgc 2869

Scoring table: IDENTITY: 100, Gap: 10, Gap: 10

Searched: 16154066 seqs 400774376 residues

Total number of hits satisfying chosen parameters: 32388132

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%
Listing first 45 summaries

Database: EST:
1: em_estdb1:
2: em_estdb2:
3: em_estdb3:
4: em_estdb4:
5: em_estdb5:
6: em_estdb6:
7: em_estdb7:
8: em_estdb8:
9: em_estdb9:
10: em_estdb10:
11: em_estdb11:
12: em_estdb12:
13: em_estdb13:
14: em_estdb14:
15: em_estdb15:
16: em_estdb16:
17: em_estdb17:
18: em_estdb18:
19: em_estdb19:
20: em_estdb20:
21: em_estdb21:
22: em_estdb22:
23: em_estdb23:
24: em_estdb24:
25: em_estdb25:
26: em_estdb26:
27: em_estdb27:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match length	DB ID	Description
1	506.4	17.7	574	AV600094
2	495.4	17.3	547	AV65727
3	494.2	17.2	548	AV65727
4	461.8	16.1	489	BF65399
5	454	15.8	490	BF65399
6	446.8	15.6	707	AV611460

7	432	15.1	483	10	AM669746	AM669746	113279	MA
8	430.8	15.0	447	10	AM484290	AM484290	59889	MA
9	424	14.8	542	12	BE639983	BE639983	14942	MA
10	422.4	14.7	541	10	BE67659	BE67659	155423	MA
11	411.4	14.3	484	13	B1680692	B1680692	459026	MA
12	402.4	14.0	745	13	B1184173	B1184173	UNL-P-FN	
13	398.4	13.9	2703	17	AF101616	AF101616	AF101616	
14	394.6	13.8	549	12	AF101616	AF101616	221675	MA
15	389.2	13.6	276	11	BE628593	BE628593	14942	MA
16	386.2	13.5	864	12	BE67659	BE67659	155423	MA
17	380.6	13.3	633	13	B1402610	B1402610	602626566	
18	378.6	13.2	840	10	PC67659	PC67659	155423	MA
19	377.6	13.2	493	10	AM426322	AM426322	601119	MA
20	377.2	13.1	553	13	BM030689	BM030689	495165	MA
21	374.8	13.1	916	14	BM024657	BM024657	AGENCOURT	
22	372.6	13.0	1452	11	AK018251	AK018251	Mus muscu	
23	369.6	12.9	4756	17	AB039843	AB039843	69115-070	
24	368.8	12.9	441	10	AV665726	AV665726	AV665726	
25	367.2	12.8	831	17	BH084844	BH084844	NCI-24-3	
26	366.4	12.8	795	17	AC985916	AC985916	CMC67824	
27	366	12.8	707	17	B76195	B76195	REC11-13P1	
28	365.2	12.7	851	14	BM024657	BM024657	AGENCOURT	
29	363.8	12.7	537	13	BM024657	BM024657	523363	MA
30	363.8	12.7	854	14	BM024657	BM024657	AGENCOURT	
31	362.8	12.6	840	12	BM019356	BM019356	602781559	
32	361.6	12.6	792	17	AC642358	AC642358	1M0505819	
33	360.2	12.6	366	10	AM445136	AM445136	25551	MAR
34	360.2	12.6	839	17	AC753382	AC753382	RTI-24-1	
35	359	12.5	859	17	BM036201	BM036201	PC1-24-2	
36	359	12.5	1340	11	BM036201	BM036201	PC1-24-2	
37	358.4	12.5	543	10	BM014743	BM014743	126579	MA
38	358.4	12.5	709	17	B16509	B16509	34285-10P	C
39	357.4	12.5	734	17	A2354288	A2354288	1M0093806	
40	357.2	12.5	689	17	A2353396	A2353396	1M0108815	
41	356.4	12.4	893	17	BH089300	BH089300	PC1-24-3	
42	356.2	12.4	799	17	AC280529	AC280529	CMC67824	
43	355	12.4	709	17	AC747554	AC747554	PC1-24-6	
44	354.8	12.4	760	17	A2747554	A2747554	PC1-24-6	
45	354.8	12.4	838	17	BH083966	BH083966	PC1-24-6	

ALIGNMENTS

RESULT 1
LOCUS: AV600094/c 574 bp mRNA linear EST 27-NOV-2001
DEFINITION: AV600094 Bos taurus cartilage Fetus Bos taurus cDNA clone
ACCESSION: E10CA048A02.57, mRNA sequence.
VERSION: AV600094
KEYWORDS: AV600094.1 GI:9718839
SOURCE: EST.

ORGANISM

Bos taurus
Bovidae: Bovinae: Bos.
Mammalia: Eutheria: Cetartiodactyla: Ruminantia: Pecora: Bovidae:
1 (bases 1 to 574)

REFERENCE

1 (bases 1 to 574)
Takahashi A, Hiratsuka S, Tsubota A, Suzuki H, Aoi H,
and Sugimoto Y.
Isolation of a high throughput cDNA sequencing system using
poly(A) tail-removed cDNA libraries and determination of 36,000
bovine ESTs
Nucleic Acids Res. 29 (22), E108 (2001)

TITLE

JOURNAL
MEDLINE
COMMENT

Contact: Yoshikazu Sugimoto
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Tel: 81-248-25-5641
Fax: 81-248-25-5725
Email: kazusug@ccococ.ocn.ne.jp
Single pass sequencing.

AV595123 598 bp mRNA linear EST 27-NOV-2001
 LOCUS AV595123
 DEFINITION AV595123 Bos taurus cartilage full Bos taurus cDNA clone
 EICAO17501 5', mRNA sequence.
 ACCESSION AV595123
 VERSION AV595123.1 GI:9711673
 KEYWORDS EST.
 SOURCE EST.
 ORGANISM Bos taurus
 COV. Bos taurus
 REFERENCES Mammalia, Chordata, Cetartiodactyla, Ruminantia, Bovina, Bovidae,
 Bovidae, Bovinae, Bos.
 1 (bases 1 to 598)
 Takasuga, A., Hirotsune, S., Itoh, R., Jitohzono, A., Suzuki, H., Aso, H.,
 and Sugimoto, Y.
 Establishment of a high throughput EST sequencing system using
 poly(A) tail-removed cDNA libraries and determination of 36,000
 bovine ESTs
 Nucleic Acids Res. 29 (22), E108 (2001)
 21570554
 JOURNAL MEDLINE
 COMMENT Contact: Yoshikazu Sugimoto
 Animal Genetics Division
 Shikawa Institute of Animal Genetics
 Odaiba, Nishino, Nishi-Shikawa, Fukushima 961-8061, Japan
 Tel: 81-248-25-5641
 Fax: 81-248-25-5726
 Email: kazusugi@doco.ocn.ne.jp
 Single pass sequencing.
 This clone was obtained from a polyA deleted cDNA library.
 Location/Qualifiers
 1..598
 /organism="Bos taurus"
 /db_xref="taxon:9913"
 /clone="PICAO17501"
 /clone_id="Bos taurus cartilage fetus"
 /tissue_type="cartilage"
 /dev_stage="fetus"
 /lab_host="DH10B"
 /note="Vector: pTZ19; Site_1: SalI; Site_2: NotI; Poly A
 was deleted from a NotI site"
 HASE COUNT 119 a 121 c 129 g 225 t 2 others
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 Best Local Similarity 94.0%; Pred. No. 2,3e-78;
 Matches 546; Conservative 0; Mismatches 30; Indels 5; Gaps 3;
 QY 1466 GGGTCGACATTCATCCAGCTCATAGAGATTCATCAATGATATCTTTTATATGCTGAG 1525
 DB 19 GTCCGACATTCATCCAGCTCATAGAGATTCATCAATGATATCTTTTATATGCTGAG 78
 QY 1526 TAATACCTCATTCATGATATGATACAGAGCTTTCATACATGATACAGAGCTGATACAG 1585
 DB 79 TAATACCTCATTCATGATATGATACAGAGCTTTCATACATGATACAGAGCTGATACAG 138
 QY 1586 CTAAGTCTTCTTATCTTCTTATATGAAAGATCTGATGAAAGATCTTCTTATATGCTGAG 1645
 DB 119 CTAAGTCTTCTTATCTTCTTATATGAAAGATCTGATGAAAGATCTTCTTATATGCTGAG 198
 QY 1646 GTGCTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCT 1705
 DB 106 GTGCTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCT 257
 QY 1706 TAAGGACATTCATTCATTCATTCATTCATTCATTCATTCATTCATTCATTCATTCATTC 1765
 DB 258 TAAGGACATTCATTCATTCATTCATTCATTCATTCATTCATTCATTCATTCATTCATTC 317
 QY 1766 ACTATGATTCATTCATTCATTCATTCATTCATTCATTCATTCATTCATTCATTCATTC 1825
 DB 318 ACTATGATTCATTCATTCATTCATTCATTCATTCATTCATTCATTCATTCATTCATTC 377
 QY 1826 CATTTATATTTGAGACTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCT 1885
 DB 111 CATTTATATTTGAGACTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCT 111

DB 378 CATTTATATTTGAGACTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCT 497
 QY 1886 ATAGAGTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCT 1941
 DB 497 ATAGAGTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCT 497
 QY 1942 TGTGTTGAGCTCATTCATTCATTCATTCATTCATTCATTCATTCATTCATTCATTCATTC 2001
 DB 498 TGTGTTGAGCTCATTCATTCATTCATTCATTCATTCATTCATTCATTCATTCATTCATTC 557
 QY 2002 TTTTATATTTGAGACTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCT 2042
 DB 558 TTTTATATTTGAGACTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCT 598
 RESULT 4
 LOCUS BF653999 489 bp mRNA linear EST 25-APR-2001
 DEFINITION BF653999
 ACCESSION BF653999
 VERSION BF653999.1 GI:11919131
 KEYWORDS EST.
 SOURCE EST.
 ORGANISM Bos taurus
 COV. Bos taurus
 REFERENCES Mammalia, Chordata, Cetartiodactyla, Ruminantia, Bovina, Bovidae,
 Bovidae, Bovinae, Bos.
 1 (bases 1 to 489)
 Smith, J.F., Grose, W.M., Breking, R.A., Roberts, A.J., Stone, R.T.,
 Casas, E., Wray, J.F., White, T., Cho, J., Fahrenkrug, S.G., Bennett,
 G.L., Heaton, M.P., Laegreid, W.W., Rohrer, G.A., Chitko-McKown, G.G.,
 Ferreira, J., Holt, J., Kadamchewa, S., Liang, F., Quackenbush, J., and
 Koehn, J.W.
 Sequence validation of four pooled tissue normalized bovine cDNA
 libraries and construction of a gene index for cattle
 Genome Res. 11 (4), 626-630 (2001)
 21180013
 JOURNAL MEDLINE
 COMMENT Contact: US Meat TPL
 USDA, ARS, US Meat Animal Research Center
 PO Box 166, Clay Center, NE 68933-0166, USA
 Tel: 402 762 4366
 Fax: 402 762 4390
 Email: smith@mail.marc.usda.gov
 Single pass sequencing. Bases called and all-trimmed with phred
 v0.980304.c. Vector identified by cross-match with the minusstore 18
 and -match 12 options.
 PCR primers
 FORWARD: AGGAACAGCTATGACAT
 BACKWARD: GTTTCAGATCAGCAG
 Plate: 70 row: 3 column: 20
 Seq primer: ATTACGTCAGCTATG.
 Location/Qualifiers
 1..489
 /organism="Bos taurus"
 /db_xref="taxon:9913"
 /clone="MARC 380V"
 /tissue_type="pooled"
 /lab_host="DH10B"
 /note="Vector: pCMV SPORT6; Site_1: NotI; Site_2: SalI;
 library made from pooled tissue from marrow, alveolar
 macrophage, ovary, fetal semitendinosus muscle, and fetal
 longissimus muscle."
 HASE COUNT 98 a 111 c 93 g 187 t
 ORIGIN
 Query Match 15.1%; Score 461.8; DB 12; Length 489;
 Best Local Similarity 96.5%; Pred. No. 1.5e-72;
 Matches 472; Conservative 0; Mismatches 17; Indels 0; Gaps 0;
 QY 1333 TCTTATATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1392
 DB 1 TCTTATATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 130

Shirakawa Institute of Animal Genetics
OdaKura, Nishigo, Nishi-shirakawa, Fukushima 961-8061, Japan
Tel: 81-248-25-5641
Fax: 81-248-25-5725

Email: Kazusugisawa.oca@nii.jp
Single pass sequencing.
This clone was obtained from a polyA-deleted cDNA library.

FEATURES

Location/Qualifiers
1..707
/organism="Bos taurus"
/db_xref="taxon:9913"
/clone="B10039609"
/clone_1ib="Bos taurus lung fetus"
/tissue_type="lung"
/dev_stage="fetus"
/lab_host="DH10B"
/note="Vector: p2L1; Site_1: SalI; Site_2: NotI; Poly A
was deleted from a NotI site"

BASE COUNT 142 127 152 9 276 1 19 others
ORIGIN

Query Match 15.6% Score 446.8; DB 10; Length 707;
Best Local Similarity 94.9%; Pred. No. 6.3e-70;
Matches 483; Conservative 3; Mismatches 24; Indels 2; Gaps 2;

QY 1723 CAGTTTAAAGAAATGCAACATGCTTCCATAGTGGCTGATGATTTGCTTCCCA 1782

DB 12 CAGTTTAAAGAAATGCAACATGCTTCCATAGTGGCTGATGATTTGCTTCCCA 71

QY 1783 CCACAGCTGAAGAGGCTTCTTCCACACCCCTCCACACCTTATTTTTCAGCA 1842

DB 72 CCACAGCTGAAGAGGCTTCTTCCACACCCCTCCACACCTTATTTTTCAGCA 131

QY 1843 CTTTGAATGCAATGATGATGATGATGATGATGATGATGATGATGATGATG 1901

DB 132 CTTTGAATGCAATGATGATGATGATGATGATGATGATGATGATGATGATG 191

QY 1902 CATTTCCTGCAATGATGATGATGATGATGATGATGATGATGATGATGATG 1961

DB 192 CATTTCCTGCAATGATGATGATGATGATGATGATGATGATGATGATGATG 251

QY 1962 GTCCTTTGAGAAATGCTATTTTCTTGGCCATTTTGTATTTGATTTGAGCTTAT 2021

DB 252 GTCCTTTGAGAAATGCTATTTTCTTGGCCATTTTGTATTTGATTTGAGCTTAT 311

QY 2022 TTTTGAATGCAATGATGATGATGATGATGATGATGATGATGATGATGATG 2081

DB 312 TTTTGAATGCAATGATGATGATGATGATGATGATGATGATGATGATGATG 371

QY 2082 TGTTCATTTGCTATTTTCTTCCATTCGAAGCTGCTTTCACCTTGTATTA 2141

DB 372 TGTTCATTTGCTATTTTCTTCCATTCGAAGCTGCTTTCACCTTGTATTA 421

QY 2142 TTTCTTGAATGCAATGATGATGATGATGATGATGATGATGATGATGATGATG 2200

DB 432 TTTCTTGAATGCAATGATGATGATGATGATGATGATGATGATGATGATGATG 491

QY 2201 TTTTTCGAATGATGATGATGATGATGATGATGATGATGATGATGATG 2228

DB 492 TTTTTCGAATGATGATGATGATGATGATGATGATGATGATGATGATG 519

RESULT 7
AM669746 483 bp mRNA linear EST 25-APR-2001

LOCUS 113279 MARC 180V Bos taurus cDNA 5', mRNA sequence.

DEFINITION AM669746

ACCESSION AM669746.1 GI:7526260

VERSION EST

KEYWORDS EST

SOURCE EST

ORGANISM Bos taurus

Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;

REFERENCE

1 (bases 1 to 483)
Smith T P L, Grose W M, Preking E A, Roberts A J, Stone R T,
Casas E, May J E, White J, Cho J, Laurent S, C, Bennett
S, L, Heaton M, P, Lacey W M, Rohrer G A, Chiklo-McKown C G,
Fetter G, Holt J, Karanycheva S, Huang F, Quackenbush J, and
Keefe J W.

Sequence evaluation of four pooled tissue normalised bovine cDNA
libraries and construction of a gene index for cattle
Genome Res. 11 (4), 626-630 (2001)

COMMENT

Contact: Smith TPL
USDA, ARS, US Meat Animal Research Center
PO Box 166, Clay Center, NE 68933-0166, USA
Tel: 402 762 4366
Fax: 402 762 4390

Email: smith@mail.marc.usda.gov
Single pass sequencing. Bases called and alt-trimmed with phred
v0.9b04.c. Vector identified by cross-match with the minuscore 18
and -mismatch 12 options.

PCR Primers

FORWARD: AGGAAACGCTATGACCAT
BACKWARD: GTTTCCTGATGACGACG
Primer 168 row 1 column 8
Seq primer: ATTATGCTGACCTATAC

FEATURES

Location/Qualifiers
1..483

/organism="Bos taurus"
/db_xref="taxon:9913"
/clone_1ib="MARC 180V"
/tissue_type="pooled"
/lab_host="DH10B"

/note="Vector: PCMV SPORT6; Site_1: NotI; Site_2: SalI;
library made from pooled tissue from lymph node, ovary,
fat, hypothalamus, and pituitary."

BASE COUNT

100 a 107 c 99 g 177 t

Query Match 15.1% Score 432; DB 10; Length 483;
Best Local Similarity 98.7%; Pred. No. 3e-67;
Matches 446; Conservative 0; Mismatches 5; Indels 1; Gaps 1;

QY 1519 GCGTGAATTAATGCAATGCTGATATGATGATGATGATGATGATGATGATGATG 1578

DB 1 GCGTGAATTAATGCAATGCTGATATGATGATGATGATGATGATGATGATGATG 60

QY 1579 TGGACATGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1638

DB 61 TGGACATGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 120

QY 1639 GGTACAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1698

DB 121 GGTACAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 180

QY 1699 TGGACATTAAGGCACTTATTTCCAGTTTAAAGCAATGCTGCTGCTGCTGCTG 1758

DB 181 TGGACATTAAGGCACTTATTTCCAGTTTAAAGCAATGCTGCTGCTGCTGCTG 240

QY 1759 TGGACATTAAGGCACTTATTTCCAGTTTAAAGCAATGCTGCTGCTGCTGCTG 1818

DB 241 TGGACATTAAGGCACTTATTTCCAGTTTAAAGCAATGCTGCTGCTGCTGCTG 400

QY 1819 TGTTCAGCAATTTATTTATTTGATGATGATGATGATGATGATGATGATGATG 1878

DB 301 TGTTCAGCAATTTATTTATTTGATGATGATGATGATGATGATGATGATGATG 360

QY 1879 GTACCTCAATGAGGTTT-GATTTCATTTTCCTGATGATGATGATGATGATGATG 1937

DB 361 GTACCTCAATGAGGTTTGTATTTGATGATGATGATGATGATGATGATGATG 420

QY 1938 CATGCTTTGTTAGCATGCTGATGCTTTT 1969

DB 421 CATGCTTTGTTAGCATGCTGCTTCTT 452

DB 288 TTGACCAATTACATCCACCAAGAGTGT -GCCACGACCTTTTCTGACACACCTCT 345
 QY 1822 CCAGATTATATTATTTAGACCTTTTGAATGAGAGGTAATCTGACCTGCTGTAATGTA 1881
 DB 346 CCACACCTACCCCTTTTATACCTTTTGAATGAGAGGCTTTTCTGACACATTAAGCTGTA 405
 QY 1882 CCTCATAGTGTG-TTGGATTGACCTTTTCTGATTAAGAGTGAAGTGAAGCTTTTCTAT 1940
 DB 406 CCTCATAGTGTGTTTGAATGAGCTTTTCTGATTAAGAGTGAAGTGAAGCTTTTCTAT 465
 QY 1941 GCTGTTTGAACATCTGATAGCTTTTGAAGAAATGCTATTAAGTTCCTTGGCCCA 2000
 DB 466 GCTGTTTGGCCATCTGATAGCTTTTGAAGAAATGCTATTAAGTTCCTTGGCCCA 525
 QY 2001 TTTTATTTAGTCTTTTATTTTCTGAGTGAAGTGAAGTGAAGTGAAGTGAAGTGA 2060
 DB 526 TTTTATTTAGTCTTTTATTTTCTGAGTGAAGTGAAGTGAAGTGAAGTGAAGTGA 585
 QY 2061 TGAGATTAGTCTTTTATTTTCTGAGTGAAGTGAAGTGAAGTGAAGTGAAGTGA 2120
 DB 586 GAGATTATTTTCTGAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGA 645
 QY 2121 TCTTTGACCTTGTCTAATAGTCTTTGATGCTGACAGACCTTTTAACTTAATAGCT 2180
 DB 646 TCTTTGCTGCTGCTTA-GGCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 703
 QY 2181 CCAATTTTATTTTCTGCTTTTATTTCTCAATTTCT 2216
 DB 704 CCAATTTTCTGCTTTGCTTTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 739

RESULT 13
 AF101616 2703 bp JMA 11991 GSS DE:NCV-2000
 LOCUS AF101616 Human Homo sapiens genome clone pYMB23.32SP6, DNA

DEFINITION AF101616 Human Homo sapiens genome clone pYMB23.32SP6, DNA
 ACCESSION AF101616
 VERSION AF101616.1 GI:4249719
 KEYWORDS GSS.

SOURCE human.
 ORGANISM Homo sapiens

REFERENCE
 AUTHORS Bepier, G., O'Brian, K.C., Kim, Y.C., Schreiber, G., and Pillerie, D.M.
 TITLE A 1.4-Mb high-resolution physical map and contig of chromosome segment 11p15.5 and genes in the LOR1A metastasis suppressor region

JOURNAL Genomics 55 (2), 164-175 (1999)
 MEDLINE 99134294
 COMMENT Contact: Bepier G
 Duke University Medical Center
 Box 2610, MSRB, Room 117, Durham, NC 27710, USA
 Part of a 1.4 megabase contig including the LOR1A metastasis suppressor region Bin B
 Class: unknown

FEATURES
 source 1..2703
 Location/Qualifiers

1..2703
 /organism="Homo sapiens"
 /db_xref="taxon:9606"
 /map="11p15.5"
 /clone="pYMB23.32SP6"
 /clone_lib="Human"
 /note="Vector: pMOS Blue"
 BASE COUNT 1057 a 573 c 483 g 590 t
 ORIGIN

Query Match 13.98; Score 398.4; DB 17; Length 2703;
 Best Local Similarity 70.34; P-val: 2e-61;
 Matches 592; Conservative 0; Mismatches 241; Indels 9; Gaps 4;

QY 1390 TTCTAAATCCCATATATATGCTTATAGTATATATATGCTTTCTGCTGCTTAC 1449
 DB 2393 TCTTAAATTTTCACTTATGATGATGATGATGATGATGATGATGATGATGATGATG 2334
 QY 1450 TTTCTTGTATATATATGATGATGATGATGATGATGATGATGATGATGATGATG 1509
 DB 2333 TTTCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 2274
 QY 1510 CTTTAAATGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1569
 DB 2273 ATTTTAAATGCTGATGATGATGATGATGATGATGATGATGATGATGATGATG 2214
 QY 1570 ATCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1629
 DB 2213 TATCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2154
 QY 1630 GAACATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1683
 DB 2153 AAACATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2094
 QY 1644 CAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1743
 DB 2093 CAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2034
 QY 1744 CAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1802
 DB 2033 CAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1974
 QY 1803 CCTTTCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1862
 DB 1973 CCTTTCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1914
 QY 1863 TGACTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1921
 DB 1913 TACTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1854
 QY 1922 ATGTTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1981
 DB 1853 ATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1794
 QY 1982 TATTTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 2041
 DB 1733 TATTTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1735
 QY 2042 GAGTGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2101
 DB 1734 TGAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1675
 QY 2102 TCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2161
 DB 1674 TCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1615
 QY 2162 TTTTAAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2221
 DB 1614 TCTTAAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1555
 QY 2222 GT 2223
 DB 1554 TT 1553

RESULT 14
 BF074298 557 bp mRNA 11991 GSS DE:NCV-2000
 LOCUS BF074298 557 bp mRNA 11991 GSS DE:NCV-2000
 DEFINITION BF074298 2Bov Bos laurus cDNA 5', mRNA sequence.
 ACCESSION BF074298
 VERSION BF074298.1 GI:10867809
 KEYWORDS EST.
 SOURCE Cow.
 ORGANISM Bos laurus

REFERENCE
 AUTHORS Bepier, G., O'Brian, K.C., Kim, Y.C., Schreiber, G., and Pillerie, D.M.
 TITLE A 1.4-Mb high-resolution physical map and contig of chromosome segment 11p15.5 and genes in the LOR1A metastasis suppressor region

